



HAN11D	MCHANSFKOFLAGGAAASSTAVAPIERVKLLLOVQHASKQISAEKQ	50
HAN12D	MCHANSFKOFLAGGAAASSTAVAPIERVKLLLOVQHASKQIADKQ	50
HAN13D	MCHANSFKOFLAGGAAASSTAVAPIERVKLLLOVQHASKQIADKQ	50
HAN11D	YKCHDCVRFKCCGALSFWFQALANVRYEPTQALNFAFKKVKQCLFL	100
HAN12D	YKCHDCVRFKCCGALSFWFQALANVRYEPTQALNFAFKKVKQCLFL	100
HAN13D	YKCHDCVRFKCCGALSFWFQALANVRYEPTQALNFAFKKVKQCLFL	100
HAN11D	GGVDFHCFWFFHGLASGGHMSLGFVFLDFAPIFLAADVGRFA	149
HAN12D	GGVDFHCFWFFHGLASGGHMSLGFVFLDFAPIFLAADVGRFA	150
HAN13D	GGVDFHCFWFFHGLASGGHMSLGFVFLDFAPIFLAADVGRFA	150
HAN11D	CFHFGGCGHFGSGGFGVQGVMSVQGINPRAFGVMDRFG	199
HAN12D	CFHFGGCGHFGSGGFGVQGVMSVQGINPRAFGVMDRFG	200
HAN13D	CFHFGGCGHFGSGGFGVQGVMSVQGINPRAFGVMDRFG	200
HAN11D	MLPDRHFMHMSAMHQSFAHGLSAPFDVFRFMMMSQSGHGDIM	249
HAN12D	MLPDRHFMHMSAMHQSFAHGLSAPFDVFRFMMMSQSGHGDIM	250
HAN13D	MLPDRHFMHMSAMHQSFAHGLSAPFDVFRFMMMSQSGHGDIM	250
HAN11D	YVGFDCWFFHFDGCGHFGHNSWLPQGGGFVLMVDELKFWL	298
HAN12D	YVGFDCWFFHFDGCGHFGHNSWLPQGGGFVLMVDELKFWL	299
HAN13D	YVGFDCWFFHFDGCGHFGHNSWLPQGGGFVLMVDELKFWL	299

Figure 2



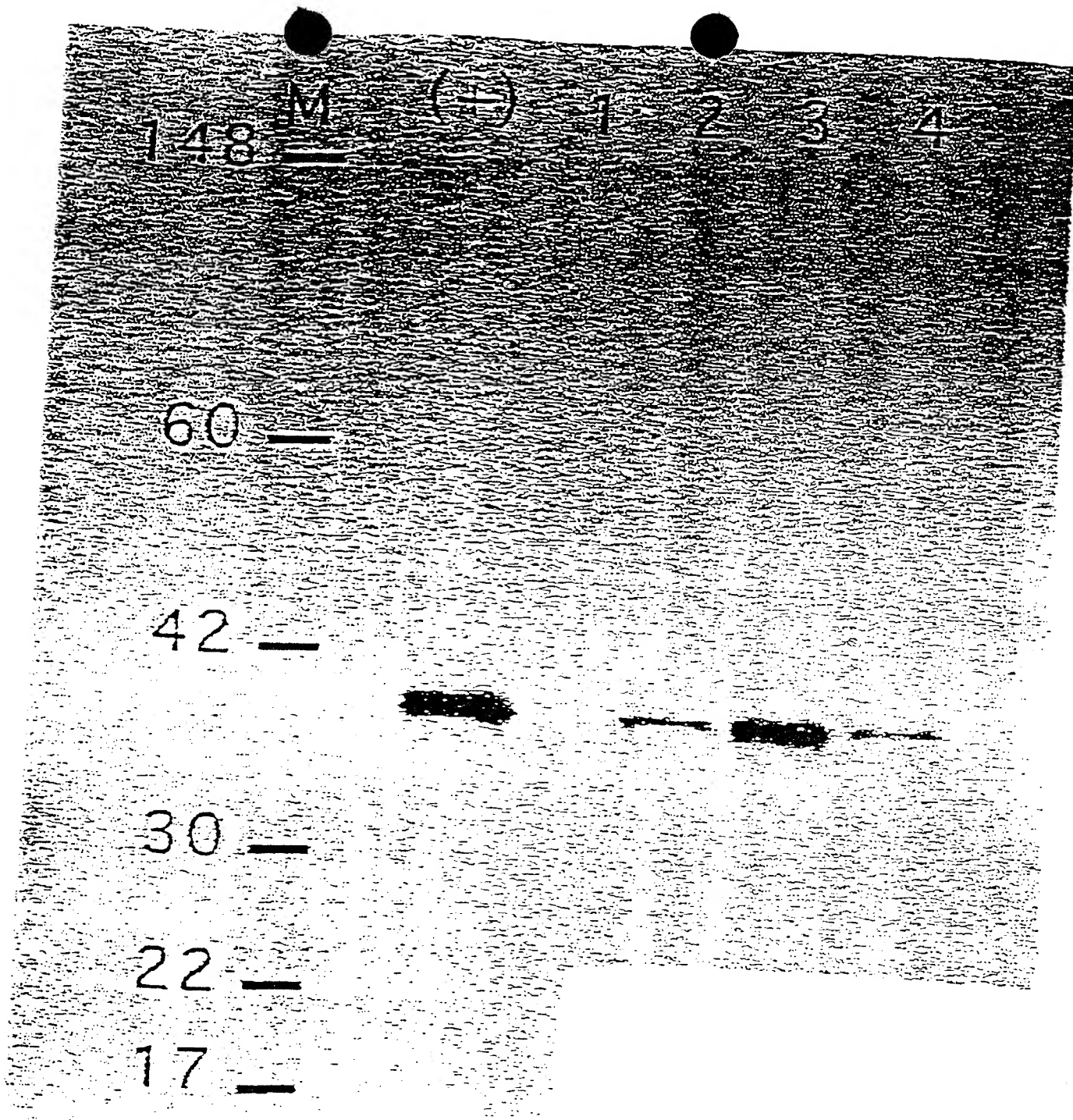


Figure 4

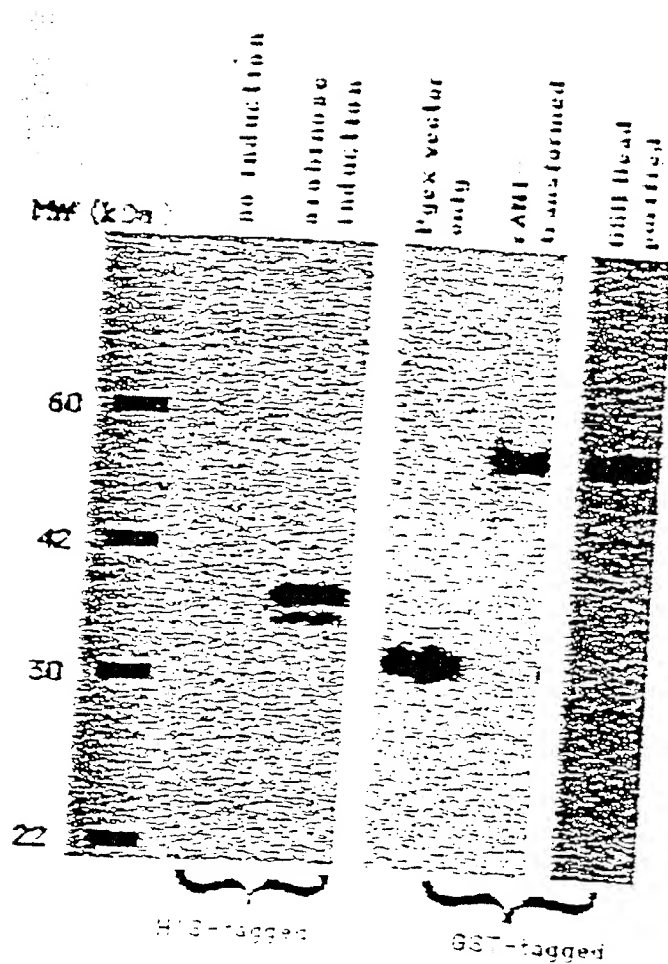


Figure 5

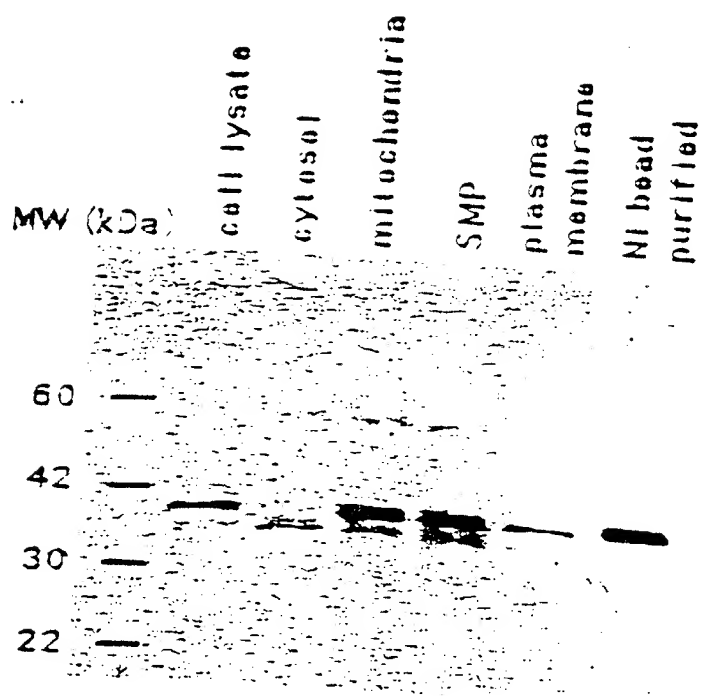


Figure 6

ATGGTCAACCCACCGTGTTCTTCGACATTGCCGTCGACGGCGAGCCCTTGGGCGCGCTCTCCTTTGAGC 70  
 TACCAGTTGGGGTGGCACAAGAAGCTGTAACGGCAGCTGCCGCTCGGGAACCCGGCGCAGAGGAAACTCG  
 M V N P T V F F D I A V D G E P L G R V S F E  
 TGTTTGCAGACAAGGTCCCAAAGACAGCAGAAAAATTTTCGTGCTCTGAGCACTGGAGAGAAAGGATTTGG 140  
 ACAAACGTCTGTTCCAGGGTTTCTGTCTCTTTTAAAAGCAGGAGACTCGTGACCTCTCTTTTCTAAACC  
 L F A D K V P K T A E N F R A L S T G E K G F G  
 TTATAAGGGTTTCCTGCTTTTCACAGAATTATTCAGGGTTTATGTGTGTCAGGGTGGTGACTTCACACGCCAT 210  
 AATATTCCTCAAGGACGAAAAGTGTCTTAATAAGGTCCCAAATACACAGTCCCACTGAAGTGTGCGGTA  
 Y K G S C F H R I I P G F M C Q G G D F T R H  
 AATGGCACTGGTGGCAAGTCCATCTATGGGGAGAAAATTTGAAGATGAGAACTTCATCCTAAAGCATACGG 280  
 TTACCGTGACCACCGTTTCAGGTAGATACCCCTCTTAAACTTCTACTCTTGAAGTAGGATTTCTATGCC  
 N G T G G K S I Y G E K F E D E N F I L K H T  
 GTCCTGGCATCTTGTCCATGGGCAAAATGCTGGACCCCAACACAAATGGTTCCTCAGTTTTTCATCTGCACTGC 350  
 CAGGACCGTAGAACAGGTACCGTTTACGACCTGGGTTGTGTACCAAGGGTCAAAAAGTAGACGTGACG  
 G P G I L S M A N A G P N T N G S Q F F I C T A  
 CAAGACTGAGTGGTTGGATGGCAAGCATGTGGTGTGGCAAAGTGAAAGAAGGCATGAATATTGTGGAG 420  
 GTTCTGACTCAGCAACCTACCGTTCTGACACCACAAACGTTTCACTTTCTTCCGTACTATAACACCTC  
 K T E W L D G K H V V F G K V K E G M N I V E  
 GCCATGGAGCGCTTTGGGTCCAGGAATGGCAAGACGAGCAAGAAGATCACCATTGCTGACTGTGGACAAC 490  
 CGGTACCTCGCGAAACCCAGGTCTTACCGTTCTGGTCTCTCTAGTGGTAACGACTGACACCTGTTG  
 A M E R F G S R N G K T S K K I T I A D C G Q  
 TCGAATAA 498  
 AGCTTATT  
 L E

Figure 7

500  
400  
300  
200  
100  
0

ATGCTGGCGCTGCGCTGCGGCTCCCGCTGGCTCGGCCTGCTCTCCGTCCCGCGCTCCGTGCCGCTGCGCC 70  
TACGACCGCGACGCGACGCGGAGGGCGACCGAGCGGACGAGAGGCAGGGCGCGAGGCACGGCGACGCGG  
M L A L R C G S R W L G L L S V P R S V P L R

TCCCGCGGCCCCGCGCCTGCAGCAAGGGCTCCCGGACCGCTCTCTTCTCTCTCTCCGGGAACCCGCT 140  
AGGGGCGCGCGGCGCGGACGTCGTTCCCGAGGCGCTGGGCAGGAGAAGGAGGAGGAGGCCCTTGGGCGA  
L P A A R A C S K G S G D P S S S S S S G N P L

CGTGTACCTGGACGTGGACGCCAACGGGAAGCCGCTCGGCCGCGTGGTGTCTGGAGCTGAAGGCAGATGTC 210  
GCACATGGACCTGCACCTGCGGTTGCCCTTCGGCGAGCCGGCGCACCACGACCTCGACTTCCGTCTACAG  
V Y L D V D A N G K P L G R V V L E L K A D V

GTCCCAAAGACAGCTGAGAACTTCAGAGCCCTGTGCACTGGTGAGAAGGGCTTCGGCTACAAAGGCTCCA 280  
CAGGGTTTCTGTGCACTCTTGAAGTCTCGGGACACGTGACCCTCTTCCCGAAGCCGATGTTTCCGAGGT  
V P K T A E N F R A L C T G E K G F G Y K G S

CCTTCCACAGGGTGATCCCTTCCTTCATGTGCCAGGCGGGCGACTTCACCAACCACAATGGCACAGGGCGG 350  
GGAAGGTGTCCCACTAGGGAAGGAAGTACACGGTCCGCGCGCTGAAGTGGTTGGTGTACCGTGTCCGCG  
T F H R V I P S F M C C A G D F T N H N G T G G

GAAGTCCATCTACGGAAGCCGCTTTCCTGACGAGAACCTTACACTGAAGCACGTGGGGGCCAGGTGTCTTG 420  
CTTCAGGTAGATGCCTTCGGCGAAAAGGACGCTCTTGAATGTGACTTCGTGCACCCCGGTCCACAGGAC  
K S I Y G S R F P D E N F T L K H V G P G V L

TCCATGGCTAATGCTGGTCCCTAACACCAACGGGTCCGAGTCTTTCATCTGCACCAATAAGACAGACTGGT 490  
AGGTACCGATTACGACCAGGATTGTGGTTGCCGAGGGTCAAGAAGTAGACGTGGTATTTCTGTCTGACCA  
S M A N A G P N T N G S C F F I C T I K T D W

TGGATGGCAAGCATGTTGTGTTCCGCTCAGGTCAAAGAGGGGCATGGACGTGCTGAAGAAAAATAGAATCTTT 560  
ACCTACCGTTCTGACAAACACAAGCCAGTGCAGTTTCTCCCGTACCTGCAGCACTTCTTTTATCTTAGAAA  
L D G K H V V F G H V K E G M D V V K K I E S F

CGGCTCTAAGAGTGGGAGGACATCCAAGAAGATTGTATCACAGACTGTGGCCAGTTGAGCTAA 624  
GCCGAGATTCTCACCCCTCCTGTAGGTTCTTCTAACAGTAGTGTCTGACACCGGTCAACTCGATT  
G S K S G R T S K K I V I T D C G Q L S

Figure 8

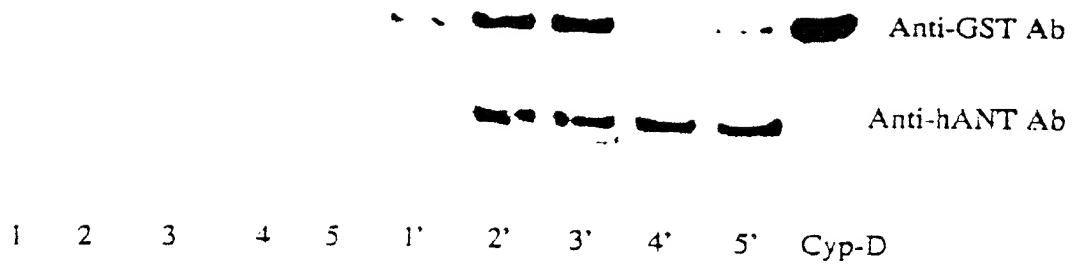


Figure 9

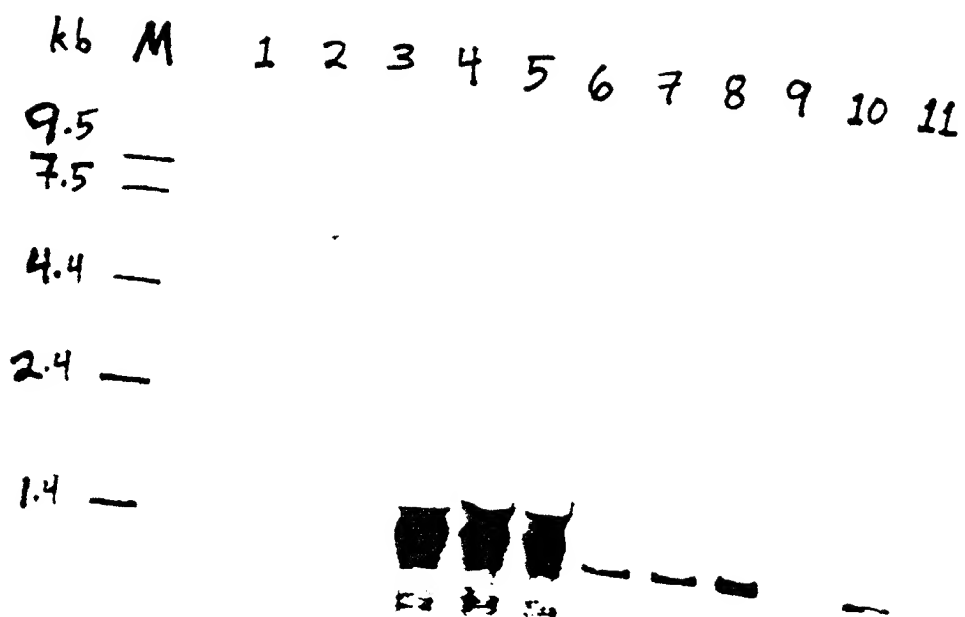


Figure 10

Control  
(no SMP)

50

100

 $+CSA$ 
$$+CSA$$
 $+ \text{CSA}$ 

GST-CypD

**Endogenes  
CypD**



Q

5

10

9

GST-CypD standards

**$\alpha$ -CypD**

FIGURE 11

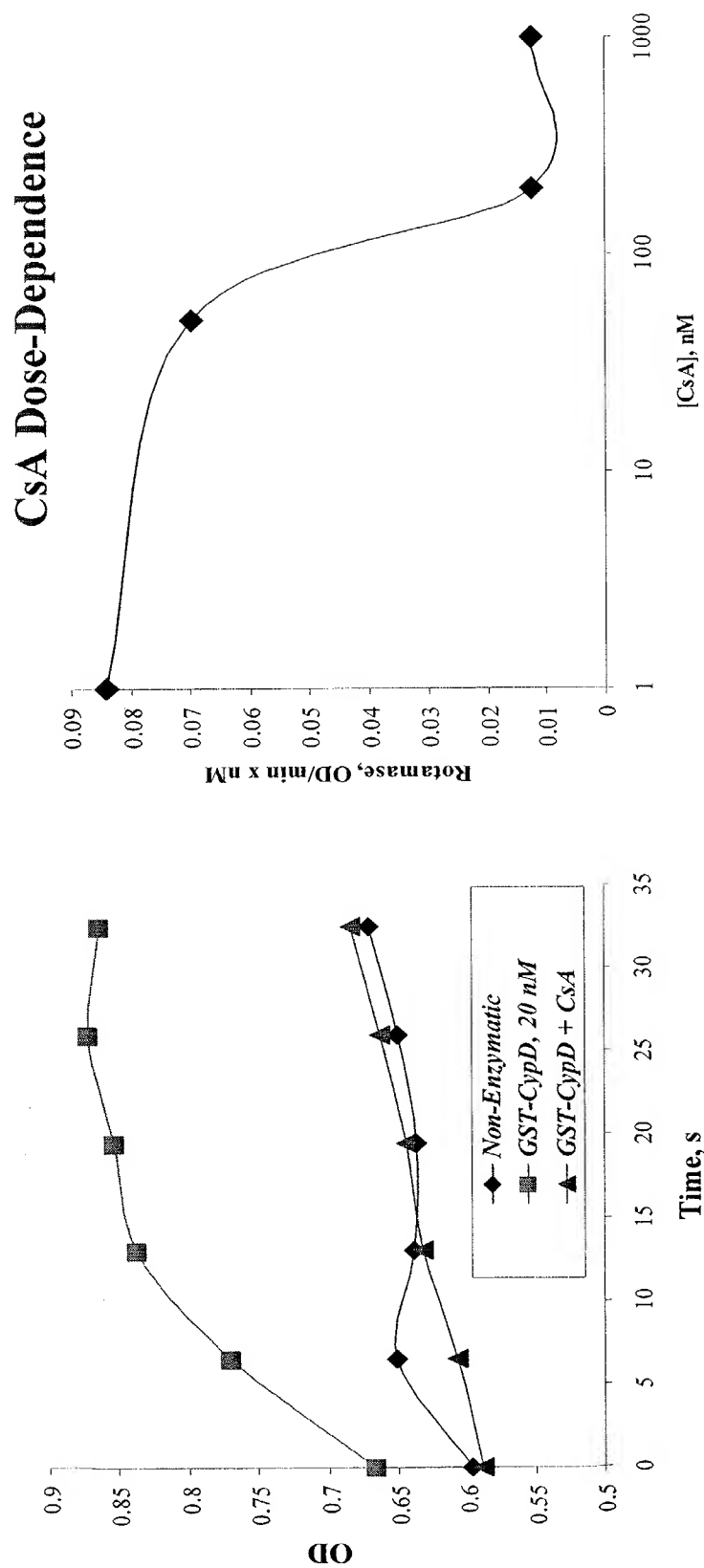


FIGURE 12

0.12  
0.1  
0.08  
0.06  
0.04  
0.02  
0

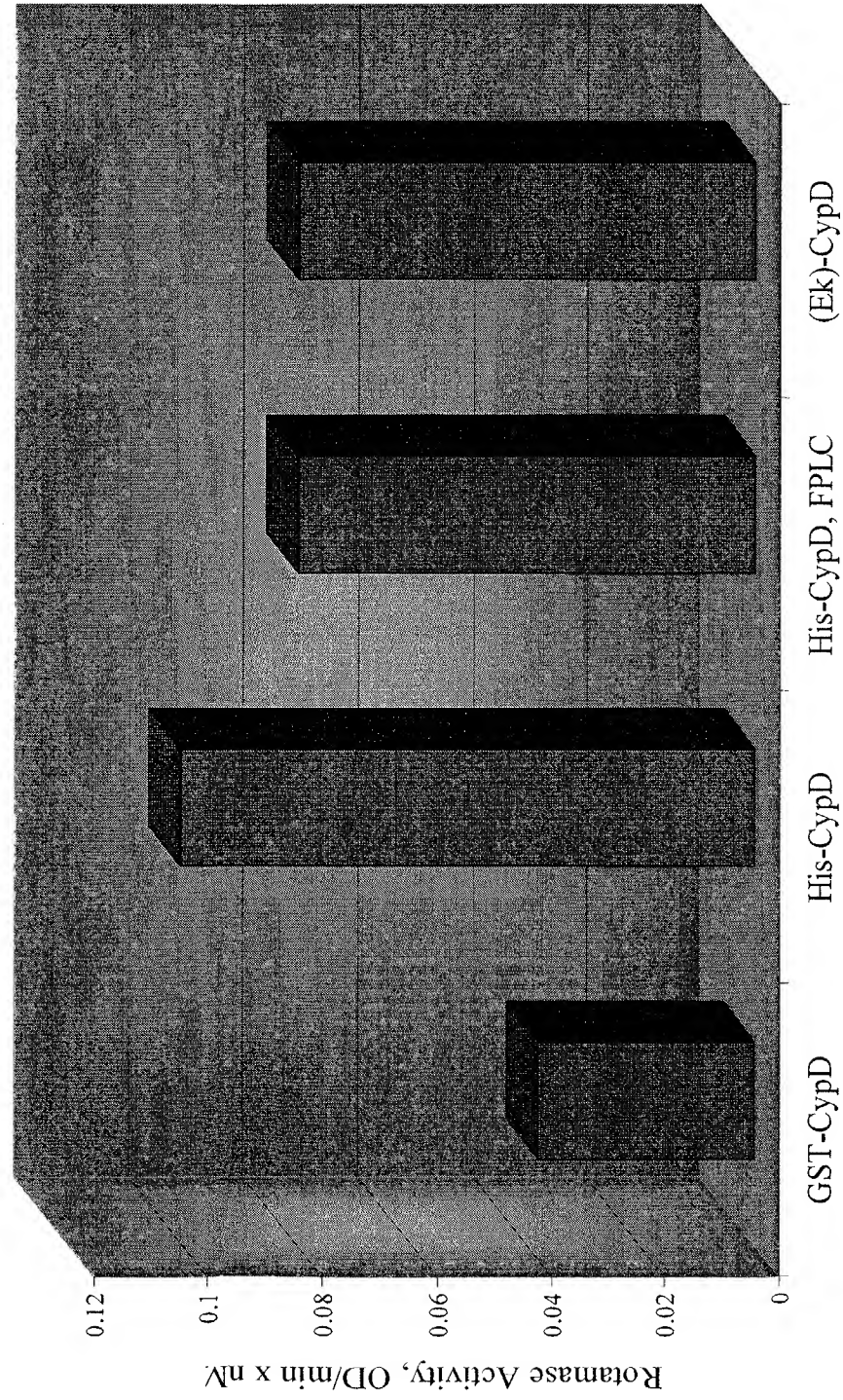


FIGURE 13

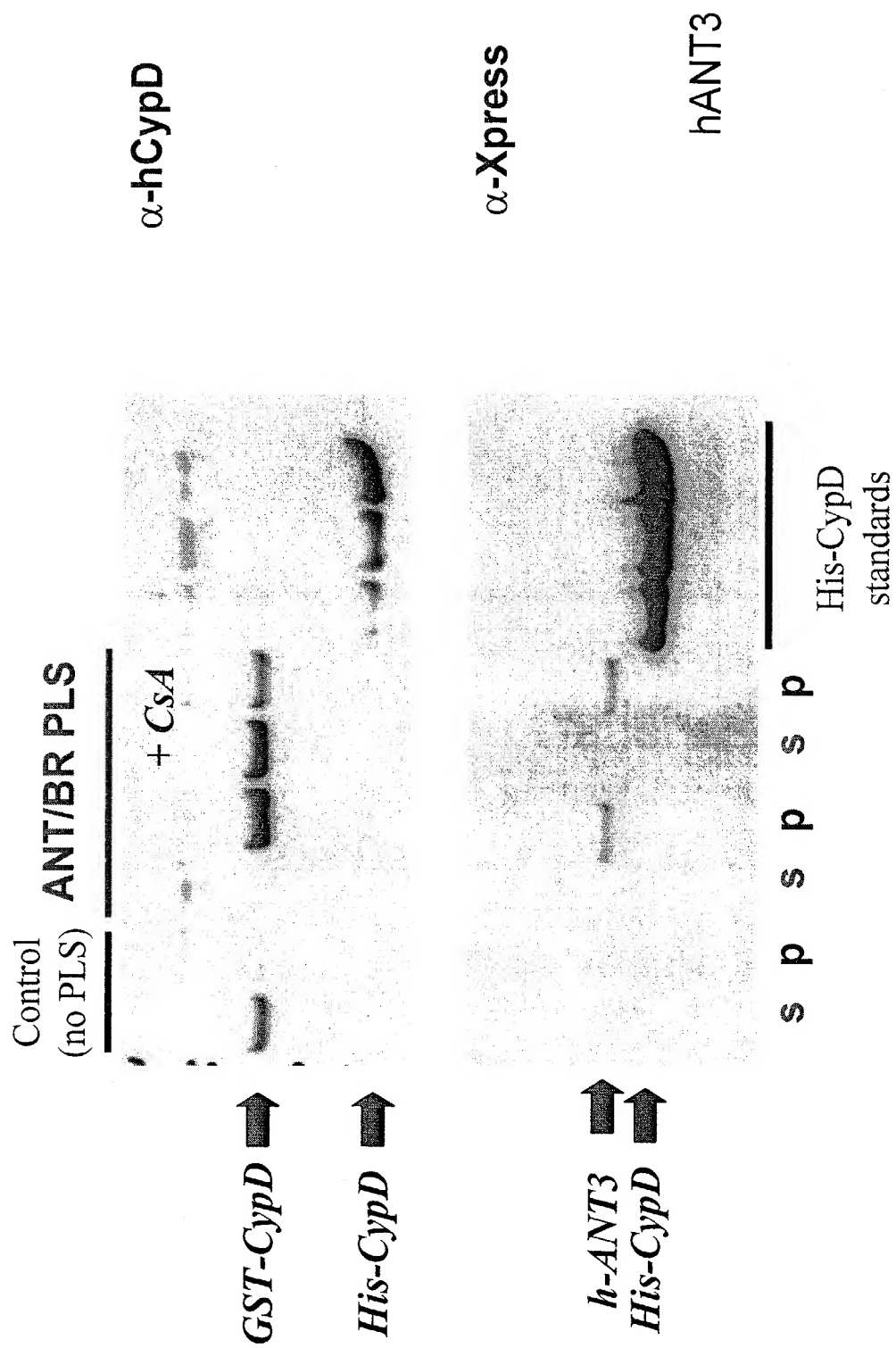


FIGURE 14

100 kDa  
 75 kDa  
 50 kDa  
 25 kDa

$\alpha$ -hCypD

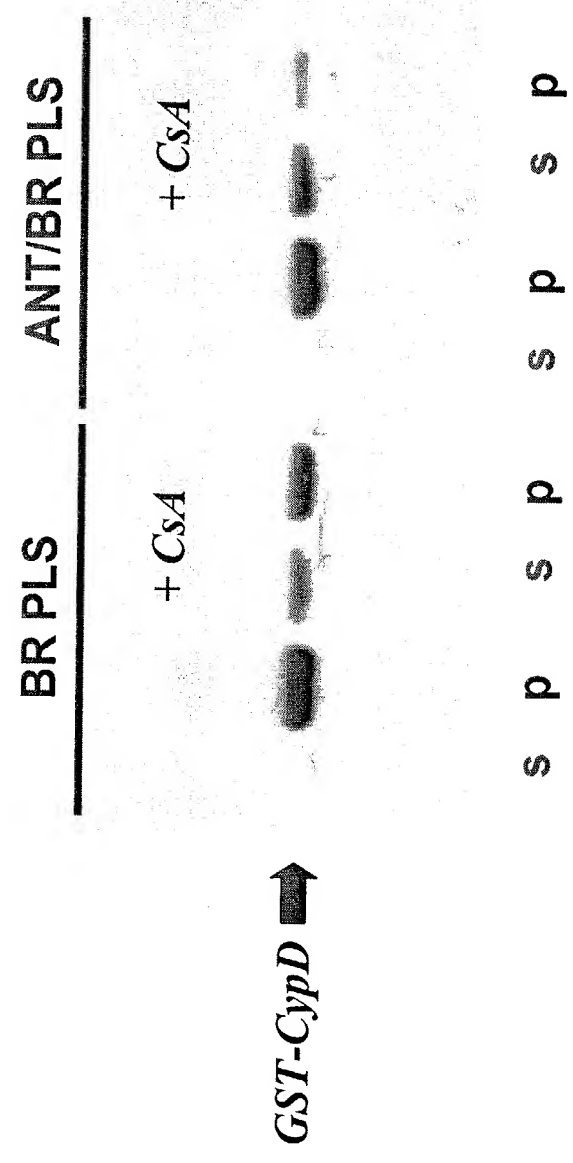


FIGURE 15